

Shalew
Paper #5

ENTERED PCT10

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/019,048

DATE: 04/10/2002

TIME: 13:09:08

Input Set : A:\019048.dos

Output Set: N:\CRF3\04102002\J019048.raw

4 <110> APPLICANT: Heinz, Ernst
 5 Girke, Thomas
 6 Scheffler, Jodi
 7 Da Costa e Silva, Oswaldo
 9 <120> TITLE OF INVENTION: Plants expressing 6-desaturase genes, PUFAS-containing oils
 from these
 10 plants, and a process for the preparation of unsaturated fatty acids
 12 <130> FILE REFERENCE: 0093/000032
 W--> 13 <140> CURRENT APPLICATION NUMBER: US 10/019,048
 C--> 14 <141> CURRENT FILING DATE: 2002-03-19
 16 <150> PRIOR APPLICATION NUMBER: PCT/EP00/006223
 17 <151> PRIOR FILING DATE: 2000-07-04
 19 <160> NUMBER OF SEQ ID NOS: 2
 21 <170> SOFTWARE: WordPerfect version 6.1
 25 <210> SEQ ID NO: 1
 27 <211> LENGTH: 2012
 29 <212> TYPE: DNA
 31 <213> ORGANISM: Physcomitrella patens
 35 <220> FEATURE:
 37 <221> NAME/KEY: CDS
 39 <222> LOCATION: (319)..(1896)
 43 <400> SEQUENCE: 1
 45 ccgagtcgcg gatcagccat cgcccgccca gggccgcctg cattgtgtgg gacgggtgttg 60
 47 gaggaggagg cagatgcgcg ggcgttggtg gagtcgtcat ccgaggatct actgcggcaa 120
 49 tacctccggg ttttgagcgg ggcaaactct gttgcggctc ggaaggctat aggttcggca 180
 51 ggagactgtt gattttatgt cgggggcatt gccattgtgg agagcggggg agactcagga 240
 53 tctgtgagtg tgcgtgcagc gcccgcactg ccgcagagcg tctgtgtatg acgaggttgt 300
 55 tgtggagcgg cttttgaa atg gta ttc gcg ggc ggt gga ctt cag cag ggc 351
 56 Met Val Phe Ala Gly Gly Gly Leu Gln Gln Gly
 57 1 5 10
 59 tct ctc gaa gaa aac atc gac gtc gag cac att gcc agt atg tct ctc 399
 60 Ser Leu Glu Glu Asn Ile Asp Val Glu His Ile Ala Ser Met Ser Leu
 61 15 20 25
 63 ttc agc gac ttc ttc agt tat gtg tct tca act gtt ggt tcg tgg agc 447
 64 Phe Ser Asp Phe Phe Ser Tyr Val Ser Ser Thr Val Gly Ser Trp Ser
 65 30 35 40
 67 gta cac agt ata caa cct ttg aag cgc ctg acg agt aag aag cgt gtt 495
 68 Val His Ser Ile Gln Pro Leu Lys Arg Leu Thr Ser Lys Lys Arg Val
 69 45 50 55
 71 tcg gaa agc gct gcc gtg caa tgt ata tca gct gaa gtt cag aga aat 543
 72 Ser Glu Ser Ala Ala Val Gln Cys Ile Ser Ala Glu Val Gln Arg Asn
 73 60 65 70 75
 75 tcg agt acc cag gga act gcg gag gca ctc gca gaa tca gtc gtg aag 591
 76 Ser Ser Thr Gln Gly Thr Ala Glu Ala Leu Ala Glu Ser Val Val Lys

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77		80		85		90	
79	ccc acg aga cga agg tca tct cag tgg aag aag tcg aca cac ccc cta	639					
80	Pro Thr Arg Arg Arg Ser Ser Gln Trp Lys Lys Ser Thr His Pro Leu						
81		95		100		105	
83	tca gaa gta gca gta cac aac aag cca agc gat tgc tgg att gtt gta	687					
84	Ser Glu Val Ala Val His Asn Lys Pro Ser Asp Cys Trp Ile Val Val						
85		110		115		120	
87	aaa aac aag gtg tat gat gtt tcc aat ttt gcg gac gag cat ccc gga	735					
88	Lys Asn Lys Val Tyr Asp Val Ser Asn Phe Ala Asp Glu His Pro Gly						
89		125		130		135	
91	gga tca gtt att agt act tat ttt gga cga gac ggc aca gat gtt ttc	783					
92	Gly Ser Val Ile Ser Thr Tyr Phe Gly Arg Asp Gly Thr Asp Val Phe						
93	140		145		150		155
95	tct agt ttt cat gca gct tct aca tgg aaa att ctt caa gac ttt tac	831					
96	Ser Ser Phe His Ala Ala Ser Thr Trp Lys Ile Leu Gln Asp Phe Tyr						
97		160		165		170	
99	att ggt gac gtg gag agg gtg gag ccg act cca gag ctg ctg aaa gat	879					
100	Ile Gly Asp Val Glu Arg Val Glu Pro Thr Pro Glu Leu Lys Asp						
101		175		180		185	
103	ttc cga gaa atg aga gct ctt ttc ctg agg gag caa ctt ttc aaa agt	927					
104	Phe Arg Glu Met Arg Ala Leu Phe Leu Arg Glu Gln Leu Phe Lys Ser						
105		190		195		200	
107	tcg aaa ttg tac tat gtt atg aag ctg ctc acg aat gtt gct att ttt	975					
108	Ser Lys Leu Tyr Tyr Val Met Lys Leu Leu Thr Asn Val Ala Ile Phe						
109		205		210		215	
111	gct gcg agc att gca ata ata tgt tgg agc aag act att tca gcg gtt	1023					
112	Ala Ala Ser Ile Ala Ile Ile Cys Trp Ser Lys Thr Ile Ser Ala Val						
113	220		225		230		235
115	ttg gct tca gct tgt atg atg gct ctg tgt ttc caa cag tgc gga tgg	1071					
116	Leu Ala Ser Ala Cys Met Met Ala Leu Cys Phe Gln Gln Cys Gly Trp						
117		240		245		250	
119	cta tcc cat gat ttt ctc cac aat cag gtg ttt gag aca cgc tgg ctt	1119					
120	Leu Ser His Asp Phe Leu His Asn Gln Val Phe Glu Thr Arg Trp Leu						
121		255		260		265	
123	aat gaa gtt gtc ggg tat gtg atc ggc aac gcc gtt ctg ggg ttt agt	1167					
124	Asn Glu Val Val Gly Tyr Val Ile Gly Asn Ala Val Leu Gly Phe Ser						
125		270		275		280	
127	aca ggg tgg tgg aag gag aag cat aac ctt cat cat gct gct cca aat	1215					
128	Thr Gly Trp Trp Lys Glu Lys His Asn Leu His His Ala Ala Pro Asn						
129		285		290		295	
131	gaa tgc gat cag act tac caa cca att gat gaa gat att gat act ctc	1263					
132	Glu Cys Asp Gln Thr Tyr Gln Pro Ile Asp Glu Asp Ile Asp Thr Leu						
133	300		305		310		315
135	ccc ctc att gcc tgg agc aag gac ata ctg gcc aca gtt gag aat aag	1311					
136	Pro Leu Ile Ala Trp Ser Lys Asp Ile Leu Ala Thr Val Glu Asn Lys						
137		320		325		330	
139	aca ttc ttg cga atc ctc caa tac cag cat ctg ttc ttc atg ggt ctg	1359					
140	Thr Phe Leu Arg Ile Leu Gln Tyr Gln His Leu Phe Phe Met Gly Leu						
141		335		340		345	

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143 tta ttt ttc gcc cgt ggt agt tgg ctc ttt tgg agc tgg aga tat acc 1407
144 Leu Phe Phe Ala Arg Gly Ser Trp Leu Phe Trp Ser Trp Arg Tyr Thr
145          350          355          360
147 tct aca gca gtg ctc tca cct gtc gac agg ttg ttg gag aag gga act 1455
148 Ser Thr Ala Val Leu Ser Pro Val Asp Arg Leu Leu Glu Lys Gly Thr
149          365          370          375
151 gtt ctg ttt cac tac ttt tgg ttc gtc ggg aca gcg tgc tat ctt ctc 1503
152 Val Leu Phe His Tyr Phe Trp Phe Val Gly Thr Ala Cys Tyr Leu Leu
153 380          385          390          395
155 cct ggt tgg aag cca tta gta tgg atg gcg gtg act gag ctc atg tcc 1551
156 Pro Gly Trp Lys Pro Leu Val Trp Met Ala Val Thr Glu Leu Met Ser
157          400          405          410
159 ggc atg ctg ctg ggc ttt gta ttt gta ctt agc cac aat ggg atg gag 1599
160 Gly Met Leu Leu Gly Phe Val Phe Val Leu Ser His Asn Gly Met Glu
161          415          420          425
163 gtt tat aat tct tct aaa gaa ttc gtg agt gca cag atc gta tcc aca 1647
164 Val Tyr Asn Ser Ser Lys Glu Phe Val Ser Ala Gln Ile Val Ser Thr
165          430          435          440
167 cgg gat atc aaa gga aac ata ttc aac gac tgg ttc act ggt ggc ctt 1695
168 Arg Asp Ile Lys Gly Asn Ile Phe Asn Asp Trp Phe Thr Gly Gly Leu
169          445          450          455
171 aac agg caa ata gag cat cat ctt ttc cca aca atg ccc agg cat aat 1743
172 Asn Arg Gln Ile Glu His His Leu Phe Pro Thr Met Pro Arg His Asn
173 460          465          470          475
175 tta aac aaa ata gca cct aga gtg gag gtg ttc tgt aag aaa cac ggt 1791
176 Leu Asn Lys Ile Ala Pro Arg Val Glu Val Phe Cys Lys Lys His Gly
177          480          485          490
179 ctg gtg tac gaa gac gta tct att gct acc ggc act tgc aag gtt ttg 1839
180 Leu Val Tyr Glu Asp Val Ser Ile Ala Thr Gly Thr Cys Lys Val Leu
181          495          500          505
183 aaa gca ttg aag gaa gtc gcg gag gct gcg gca gag cag cat gct acc 1887
184 Lys Ala Leu Lys Glu Val Ala Glu Ala Ala Glu Gln His Ala Thr
185          510          515          520
187 acc agt taa cagtctttgg aaagcttggc aattgatctt tattctccac 1936
188 Thr Ser
189          525
191 ggcagttgct tgtttgtttt ggggtgaatg accgaatgta ctggcatcca ttctttctgta 1996
193 gccatcaatt ttgaac 2012
197 <210> SEQ ID NO: 2
199 <211> LENGTH: 525
201 <212> TYPE: PRT
203 <213> ORGANISM: Physcomitrella patens
205 <400> SEQUENCE: 2
207 Met Val Phe Ala Gly Gly Gly Leu Gln Gln Gly Ser Leu Glu Glu Asn
208 1          5          10          15
210 Ile Asp Val Glu His Ile Ala Ser Met Ser Leu Phe Ser Asp Phe Phe
211          20          25          30
213 Ser Tyr Val Ser Ser Thr Val Gly Ser Trp Ser Val His Ser Ile Gln
214          35          40          45

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216 Pro Leu Lys Arg Leu Thr Ser Lys Lys Arg Val Ser Glu Ser Ala Ala
217      50      55      60
219 Val Gln Cys Ile Ser Ala Glu Val Gln Arg Asn Ser Ser Thr Gln Gly
220 65      70      75      80
222 Thr Ala Glu Ala Leu Ala Glu Ser Val Val Lys Pro Thr Arg Arg Arg
223      85      90      95
225 Ser Ser Gln Trp Lys Lys Ser Thr His Pro Leu Ser Glu Val Ala Val
226      100      105      110
228 His Asn Lys Pro Ser Asp Cys Trp Ile Val Val Lys Asn Lys Val Tyr
229      115      120      125
231 Asp Val Ser Asn Phe Ala Asp Glu His Pro Gly Gly Ser Val Ile Ser
232      130      135      140
234 Thr Tyr Phe Gly Arg Asp Gly Thr Asp Val Phe Ser Ser Phe His Ala
235 145      150      155      160
237 Ala Ser Thr Trp Lys Ile Leu Gln Asp Phe Tyr Ile Gly Asp Val Glu
238      165      170      175
240 Arg Val Glu Pro Thr Pro Glu Leu Leu Lys Asp Phe Arg Glu Met Arg
241      180      185      190
243 Ala Leu Phe Leu Arg Glu Gln Leu Phe Lys Ser Ser Lys Leu Tyr Tyr
244      195      200      205
246 Val Met Lys Leu Leu Thr Asn Val Ala Ile Phe Ala Ala Ser Ile Ala
247      210      215      220
249 Ile Ile Cys Trp Ser Lys Thr Ile Ser Ala Val Leu Ala Ser Ala Cys
250 225      230      235      240
252 Met Met Ala Leu Cys Phe Gln Gln Cys Gly Trp Leu Ser His Asp Phe
253      245      250      255
255 Leu His Asn Gln Val Phe Glu Thr Arg Trp Leu Asn Glu Val Val Gly
256      260      265      270
258 Tyr Val Ile Gly Asn Ala Val Leu Gly Phe Ser Thr Gly Trp Trp Lys
259      275      280      285
261 Glu Lys His Asn Leu His His Ala Ala Pro Asn Glu Cys Asp Gln Thr
262      290      295      300
264 Tyr Gln Pro Ile Asp Glu Asp Ile Asp Thr Leu Pro Leu Ile Ala Trp
265 305      310      315      320
267 Ser Lys Asp Ile Leu Ala Thr Val Glu Asn Lys Thr Phe Leu Arg Ile
268      325      330      335
270 Leu Gln Tyr Gln His Leu Phe Phe Met Gly Leu Leu Phe Phe Ala Arg
271      340      345      350
273 Gly Ser Trp Leu Phe Trp Ser Trp Arg Tyr Thr Ser Thr Ala Val Leu
274      355      360      365
276 Ser Pro Val Asp Arg Leu Leu Glu Lys Gly Thr Val Leu Phe His Tyr
277      370      375      380
279 Phe Trp Phe Val Gly Thr Ala Cys Tyr Leu Leu Pro Gly Trp Lys Pro
280 385      390      395      400
282 Leu Val Trp Met Ala Val Thr Glu Leu Met Ser Gly Met Leu Leu Gly
283      405      410      415
285 Phe Val Phe Val Leu Ser His Asn Gly Met Glu Val Tyr Asn Ser Ser
286      420      425      430
288 Lys Glu Phe Val Ser Ala Gln Ile Val Ser Thr Arg Asp Ile Lys Gly

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289	435	440	445
291 Asn Ile Phe Asn Asp Trp Phe Thr Gly Gly Leu Asn Arg Gln Ile Glu			
292 450	455	460	
294 His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Asn Lys Ile Ala			
295 465	470	475	480
297 Pro Arg Val Glu Val Phe Cys Lys Lys His Gly Leu Val Tyr Glu Asp			
298	485	490	495
300 Val Ser Ile Ala Thr Gly Thr Cys Lys Val Leu Lys Ala Leu Lys Glu			
301	500	505	510
303 Val Ala Glu Ala Ala Ala Glu Gln His Ala Thr Thr Ser			
304	515	520	525

VERIFICATION SUMMARY

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Input Set : A:\019048.dos

Output Set: N:\CRF3\04102002\J019048.raw

L:13 M:283 W: Missing Blank Line separator, <140> field identifier

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date